IN THE CLAIMS:

Please amend the claims as follows:

1. (Currently Amended) A method including

accessing information about a plurality of gene expression values;

generating from said information a hypothesized relationship about genes relative to said information from a relationship between one or more sets of associated with said gene expression values, said hypothesized relationship having a likelihood of being due to chance not exceeding a predetermined value;

retrieving data regarding interests of each agent of a plurality of agents;

identifying at least one agent of the plurality of agents such that the data regarding interests of said at least one agent satisfies at least one predetermined test indicating that said at least one agent has a potential interest in the hypothesized relationship; and

sending information about said hypothesized relationship to said at least one agent.

2. (Previously Presented) A method as in claim 1, including collecting said information about the plurality of gene expression values from a plurality of external databases.

3. (Previously Presented) A method as in claim 1, including collecting said information from at least one external database.

4. (Original) A method as in claim 1, wherein generating includes

selecting a first set of genes in response to said gene expression values;

selecting a second set of genes in response to data other than said gene expression values;

applying a statistical technique to said first set and said second set; and

confirming said hypothesized relationship in response to applying said statistical technique.

5. (Original) A method as in claim 1, wherein generating includes

selecting a set of genes in response to said gene expression values;

comparing the frequencies of the nucleotide sequences upstream from said set of genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and

constructing a hypothesis that is responsive to sequences that have an anomalous frequency distribution.

6. (Previously Presented) A method as in claim 1, wherein generating includes

examining pathways of genes with respect to gene activation sequences;

extending said pathways using said gene expression information; and

constructing a hypothesized relationship concerning an extension of at least one of said pathways.

7. (Previously Presented) A method as in claim 1, wherein generating includes

evaluating correlation values with respect to an identified gene or gene sequence so as

to determine variations in the behavior of said identified gene or gene sequence; and

confirming said hypothesized relationship by applying a statistical technique.

8. (Previously Presented) A method as in claim 1, wherein the step of identifying

includes:

rating said hypothesized relationship with a measure of interest by said at least one

agent; and

selecting said at least one agent responsive to said measure.

9. (Previously Presented) A method as in claim 8, wherein the step of selecting

includes:

determining a threshold in said measure of interest; and

comparing said threshold and said measure of interest.

10. (Original) A method as in claim 8, wherein said measure of interest is

periodically reevaluated.

11. (Previously Presented) A method as in claim 8, wherein said measure of interest

is responsive to complexity of said hypothesized relationship, the likelihood of said hypothesized

relationship being due to chance, or whether said hypothesized relationship relates to at least one of:

genes one or more researchers have indicated they are interested in, genes for which there are

published papers, selected domain-specific knowledge about gene expression.

12. (Canceled).

13. (Previously Presented) A method as in claim 1, wherein said data regarding

interests includes at least one of: information about interests of said at least one agent, information

about published papers, information about researchers, information about relationships between

genes.

14. (Previously Presented) Apparatus including

memory recording information about a plurality of gene expression values;

an autonomous software element disposed on a computing device, said autonomous

software element having access to said memory;

said memory recording information about a hypothesized relationship between said

gene expression values, said hypothesized relationship having the properties of (1) having a

likelihood of being due to chance not exceeding a predetermined value, and (2) satisfying at least one

predetermined test indicating that said hypothesized relationship is of potential interest to at least one

agent; and

a communication link coupled to said memory and capable of sending information about said hypothesized relationship to said at least one agent.

15. (Previously Presented) Apparatus as in claim 14, wherein said communication link is capable of collecting said information about the plurality of gene expression values from a plurality of external databases.

16. (Previously Presented) Apparatus as in claim 14, wherein said communication link is capable of collecting said information from at least one external database.

17. (Original) Apparatus as in claim 14, wherein

said hypothesized relationship includes (a) information about a first set of genes, said first set of genes having been selected in response to said gene expression values, and (b) information about a second set of genes, said second set of genes having been selected in response to data other than said gene expression values;

said hypothesized relationship has been confirmed in response to a statistical technique applied to said first set and said second set.

18. (Previously Presented) An apparatus as in claim 14, including

a means for selecting a first set of genes in response to said gene expression values;

a means for selecting a second set of genes in response to data other than said gene expression values;

a means for applying a statistical technique to said first set and said second set; and

a means for confirming said hypothesized relationship in response to applying said statistical technique.

19. (Original) An apparatus as in claim 14, including

a means for selecting a set of genes in response to said gene expression values;

a means for comparing the frequencies of the nucleotide sequences upstream from said set of genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and

a means for constructing a hypothesis that is responsive to sequences that have an anomalous frequency distribution.

20. (Previously Presented) An apparatus as in claim 14, including

a means for examining pathways of genes with respect to gene activation sequences;

a means for extending said pathways using said gene expression information; and

a means for constructing a hypothesized relationship concerning an extension of at least one of said pathways.

21. (Previously Presented) An apparatus as in claim 14, including

a means for evaluating correlation values with respect to an identified gene or gene sequence so as to determine variations in the behavior of said identified gene or gene sequence; and

a means for confirming said hypothesized relationship in response to applying a statistical technique.

22. (Previously Presented) Apparatus as in claim 14, said memory including information associating said hypothesized relationship with a measure of interest by said agent; and

a software comparator coupled to said measure of interest and to a selected threshold.

23. (Original) Apparatus as in claim 14, wherein said autonomous software element has access to collateral information other than gene expression values.

24. (Previously Presented) A memory recording information including instructions, said instructions interpretable by a computing device, said instructions including

an autonomous software element having access to information about a plurality of gene expression values;

a first software element coupled to said information and capable of generating a hypothesized relationship between said gene expression values, said hypothesized relationship having the properties of (1) having a likelihood of being due to chance not exceeding a predetermined value, and (2) satisfying at least one predetermined test indicating that said

hypothesized relationship is of potential interest to at least one agent other than said autonomous software element;

a second software element coupled to information about said hypothesized relationship and capable of sending information about said hypothesized relationship to said at least one agent.

25. (Original) A memory as in claim 24, including

information about a first set of genes selected in response to said gene expression values;

information about a second set of genes selected in response to data other than said gene expression values;

information about said hypothesized relationship selected in response to applying a statistical technique to said first set and said second set.

26. (Previously Presented) A memory as in claim 24, wherein generating by the first software element includes

selecting a first set of genes in response to said gene expression values;

selecting a second set of genes in response to data other than said gene expression values;

applying a statistical technique to said first set and said second set; and

confirming said hypothesized relationship in response to applying said statistical

technique.

27. (Previously Presented) A memory as in claim 24, wherein generating by the first

software element includes

selecting a set of genes in response to said gene expression values;

comparing the frequencies of the nucleotide sequences upstream from said set of

genes to the frequencies of the nucleotide sequences upstream of genes not in said set; and

constructing a hypothesis that is responsive to sequences that have an anomalous

frequency distribution.

28. (Previously Presented) A memory as in claim 24, including

information about examining pathways of genes with respect to gene activation

sequences;

information about extending said pathways using said gene expression information;

and

information about constructing a hypothesized relationship concerning an extension

of said pathways.

29. (Previously Presented) A memory as in claim 24, wherein the first software

element

evaluates correlation values with respect to an identified gene or gene sequence so as to determine variations in the behavior of said identified gene or gene sequence; and

confirms said hypothesized relationship in response to applying a statistical technique.

30. (Currently Amended) A method including

accessing information about a set of genes and proteins;

generating from said information a hypothesized relationship involving at least one of the following: a set of proteins, SNPs and chemicals pertaining to said information, said hypothesized relationship relative to said information and having a likelihood of being due to chance not exceeding a predetermined value;

retrieving data regarding interests of each agent of a plurality of agents;

identifying at least one agent of the plurality of agents such that the data regarding interests of said at least one agent satisfies at least one predetermined test indicating that said at least one agent has a potential interest in the hypothesized relationship; and

sending information about said hypothesized relationship to said at least one agent.

31. (Previously Presented) A method as in claim 30, including collecting said information from a plurality of external databases.

32. (Previously Presented) A method as in claim 30, including collecting said information from at least one external database.

33. (Previously Presented) A method as in claim 30, wherein the step of identifying includes:

rating said hypothesized relationship with a measure of interest by said at least one agent; and

selecting said at least one agent responsive to said measure.

34. (Previously Presented) A method as in 33, wherein the step of selecting includes:

determining a threshold in said measure of interest; and

comparing said threshold and said measure of interest.

35. (Original) A method as in claim 34, wherein said measure of interest is periodically reevaluated.

36. (Canceled)

37. (Previously Presented) A method as in claim 34, wherein said data regarding interests includes at least one of: information about interests of said at least one agent, information about published papers, information about researchers, information about relationships between genes.